What is claimed is:

1. A modified DNA cleaving enzyme, comprising:

(a) at least 35% amino acid sequence identity with T7 Endo I,

(b) two catalytic centers separated by a β-bridge, and

(c) at least one mutation in the β-bridge that has an effect of altering enzyme cleavage activity compared to the unmodified enzyme.

2. A modified DNA cleaving enzyme according to claim 1, having reduced toxicity in a host cell permitting over-expression of the DNA cleaving enzyme.

3. A modified DNA cleaving enzyme according to claim 1, wherein the enzyme activity comprises at least one of: cleavage at a cruciform structure on DNA, non-sequence specific nicking, nicking opposite a pre-existing nick site, non-sequence specific DNA cleavage and cleavage of DNA at a site flanking a mismatch base pair.

4. A modified DNA cleaving enzyme according to claim 1, wherein the product of the altered enzyme activity is a DNA duplex with a single strand over-hang of less than 11 nucleotides.

5. A modified DNA cleaving enzyme according to claim 1, wherein the altered enzyme cleavage activity further comprises a broadened enzyme specificity compared with the unmodified enzyme.

6. A modified DNA cleaving enzyme according to claim 5, wherein the DNA cleaving activity further comprises cleaving at a mismatch

in a duplex where the mismatch can be any of an A, T, G or C bases.

7. An A modified DNA cleaving enzyme according to claim 1, wherein an alteration in the enzyme cleavage activity of the modified enzyme compared to the unmodifed enzyme occurs in a manganese-containing buffer.

8. A modified DNA cleaving enzyme according to claim 7, wherein the altered enzyme activity is selected from: maintenance of cleavage activity, reduction of non-specific nuclease activity, enhanced nicking activity opposite a pre-existing nick site, and a decreased ratio of nicking to double strand cleavage.

9. A modified DNA cleaving enzyme according to claim 1, wherein the altered enzyme activity occurs in magnesium buffer.

10. A modified DNA cleaving enzyme according to claim 9, wherein the altered enzyme activity is selected from: an increased ratio of nicking of a cruciform structure in the DNA relative to double strand cleavage; an increased ratio of cleaved DNA of a cruciform to non-cleaved DNA; a reduced ratio of non-specific nuclease activity; and reduction in nicking opposite a preexisting nick site.

11. A modified DNA cleaving enzyme according to claim 1, having enhanced or reduced activity for cleavage a DNA under modified reaction conditions when compared with the unmodified enzyme.

12. A modified DNA cleaving enzyme according to claim 12, wherein the modification in reaction conditions are selected from changing

at least one of :pH, temperature, manganese or magnesium salt concentration of the reaction mixture and time of the reaction.

13. A modified DNA cleaving enzyme according to claim 1, selected from a class of enzymes comprising: gene 3 (enterobacteriaphage T7), T7 endodeoxyribonuclease I, Yersinia pestis phage phiA1122 endonuclease, Phage Phi Ye03-12 endonuclease, Phage T3 endonuclease, phage T3 endodeoxyribonuclease , Pseudomonas phage gh-1 endonuclease, psuedomonas putida KT2440 endodeoxyribonuclease I; and Roseophage S101 RP endonuclease I.

14. A modified DNA cleaving enzyme according to claim 1, wherein the at least one mutation is a mutation at a PA site in the β-bridge.

15. A modified DNA cleaving enzyme according to claim 14, wherein the at least one mutation at the PA site is a substitution of PA or deletion such that the substitution of PA is selected from a single amino acid, a dipeptide, a tripeptide and a tetrapeptide.

16. A modified DNA cleaving enzyme according to claim 15, wherein the at least one mutation in the β-bridge is selected from PA/A, PA/AA, PA/PGA, PA/PAPA, ΔPA, PA/K, PA/G, PA/D and PA/P.

17. A modified DNA cleaving enzyme according to claim 15, wherein the PA dipeptide is located at position 46 and 47 in SEQ ID. No. 13.

18. A nucleic acid comprising a DNA sequence that substantially corresponds to SEQ ID NO:1 wherein at least one mutation has been introduced in the sequence corresponding to the β-bridge.

19. The nucleic acid according to claim 18, wherein the mutation occurs at a site which encodes the PA in the β-bridge.

20. The nucleic acid according to claim 19, wherein the mutation at the site that encodes PA is a substitution or deletion such that the substituted nucleic acid encodes a single amino acid, a dipeptide, a tripeptide and a tetrapeptide.

21. A nucleic acid according to claim 17, wherein the at least one mutation results in an amino acid change selected from PA/A, PA/AA, PA/PGA, PA/PAPA, ΔPA, PA/K, PA/G, PA/D and PA/P.

22. A vector encoding the nucleic acid of any of claim 18 through 21.

23. A host cell containing a vector of claim 22.

24. A kit containing at least one of: a modified DNA cleaving enzyme of claim 1, a nucleic acid of claim 18-21, a vector of claim 22, or a host cell of claim 23.

25. A method for modifying enzyme catalytic activity, comprising:

(a) selecting an enzyme having two catalytic centers connected by a β-bridge, the catalytic centers being located at reciprocal stereo-geometric positions in the enzyme;

(b) changing the reciprocal stereo-geometric position of the two catalytic centers by introducing a mutation into the β-bridge; and

(c) modifying the catalytic activity of the enzyme.

26. A method of determining whether a DNA substrate has a single nucleotide polymorphism (SNP), comprising:

(a) contacting the DNA substrate with a modified DNA cleaving enzyme according to claim 1; and

(b) determining from the cleavage product whether the DNA substrate has the SNP.

27. A method according to claim 26, further comprising: identifying which nucleotide forms the SNP.

28. A method according to claim 26, further comprising: identifying the location of the SNP.

29. A method of forming a shotgun cloning library, comprising

(a) incubating a modified DNA cleaving enzyme according to claim 1 with a DNA to form non-sequence specific cleavage fragments of the DNA that are ligatable; the ligatable DNA being capable of insertion into a vector for cloning in a host cell; and

(b) forming the shotgun cloning library.

30. A method for mapping nicks in a duplex DNA, comprising;

(a) incubating a modified DNA cleaving enzyme according to claim 1 with the duplex DNA in a manganese-containing buffer;

(b) permitting nicking to occur across from a pre-existing nick site to form fragments of the duplex DNA with single strand overhangs; and

(c) mapping the nicks in the DNA.

31. A method for over-expressing T7 endonuclease 1, comprising

selecting a host cell according to claim 23 and over-expressing the T7 endonuclease 1.